

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:08:26 ; Search time 54.19 Seconds

(without alignments)

383.293 Million cell updates/sec  
 383.293 Million cell updates/sec

Title: US-09-772-103-10

Sequence: 1 MAVLVLFCLVAFPSCVLSQ . . . . . MKRGYAMDYWGQGTLYTVSS 142

Scoring table: BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Actual number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL17:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rhodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.: Score Match Length DB ID Description

1 462.5 62.3 121 11 Q99NG4

2 43.7 58.9 119 4 Q9UL73

3 43.5 58.7 150 4 Q95973

4 42.9 57.8 597 4 Q9BU10

5 42.7 57.5 597 4 Q9BQB8

6 39.2 52.9 479 11 Q99M22

7 37.4 50.4 121 4 Q9UL96

8 34.6 46.7 122 4 Q9UL75

9 34.5 46.4 112 4 Q9HCC1

10 32.6 43.9 116 4 Q9UL93

11 32.3 43.5 113 4 Q9UL90

12 32.3 43.5 131 4 Q9UL88

13 32.1 43.3 121 4 Q9UL71

14 319.5 43.1 124 4 Q9UL92

15 318.5 42.9 147 4 Q9Y509

16 317.5 42.8 122 4 Q9UL84

17 317.5 42.8 487 11 Q99KA4

18 313.5 42.3 118 4 Q9UL72

19 311.5 42.0 124 6 Q9NOW6

#### ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	121 AA.
ID	Q99NG4			
AC	Q99NG4;			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
DE	SINGLE CHAIN FV (FRAGMENT).			
DE	Mus musculus (Mouse).			
OS	Mus musculus (Mouse).			
OG	Plasmid PHEN1.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN				
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RX	MEDLINE=98169018; PubMed=9510199;			
RA	Hawlicsch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,			
RA	Bautsch W., Kola A., Klos A., Koehl J.; Site-Directed C3a-Receptor Antibodies from Phage Display Libraries. ;			
RT	J. Immunol. 160:2947-2958(1998).			
RL	EMBL; AJ222590; CAA10890.1; -.			
DR				
KW	Plasmid.			
FT	NON-TER	1		
FT	SEQUENCE	121 AA; 13255 MW;	D293E4EBC8C59D5B CRC64;	
Query Match	62.3%	Score 462.5;	Length 121;	
Best Local Similarity	73.2%	Pred. No. 7.5e-39;		
Matches	90;	Conservative 10; Mismatches 20;	Indels 3;	Gaps 1;
QY	20 QVQLOESGGGLVKSQTLISCTVSGFSLTSYGVWROPGKGLEWLGIVWAGGTTNN 79			
Db	1 QVQLEKGSGGLVAPSQSLSTCNGFPLTSHGSWVROPGKGLEWLGIVWAGGTTNN 60			
QY	80 SALMSRLTLSKDTISKNOYSLKLSSVTAADTAVYCCARSGPHAMKRGYAMDYNGQGTLYT 139			
Db	61 SALISRSLSKDNISKQVFLKLNLSQTTDTATYCAR - - HYYKAYANVAMDYWGQGT SYT 117			
QY	140 VSS 142			

Db	118	VSS 120	DR EMBL; AF103795; AAC79084.1; -.
RESULT	2		DR HSSP; P01825; 7FAB.
Q9UL73	PRELIMINARY;	PRT;	DR InterPro; IPR03006; Ig_MHC.
ID Q9UL73; AC 01-MAY-2000 (TREMBLrel. 13, Created)			DR InterPro; IPR03596; Ig_v.
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			DR Pfam; PF00047; ig; Ig_v.
DT 01-MAY-2001 (TREMBLrel. 17, Last annotation update)			DR SMART; SM00406; IgV; Ig_v.
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).			KW SIGNAL.
OS Homo sapiens (Human).			KW SIGNAL.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			KW SIGNAL.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			KW SIGNAL.
OX NCBI_TAXID=9606;			FT SIGNAL.
RN [1]	SEQUENCE FROM N.A.		FT CHAIN.
RX MEDLINE=98277139; PubMed=9614934;			FT NON_TER.
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			FT 150 >150
RX Young D.C.;			SEQUENCE 150 AA; 16315 MW;
RX "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";			POTENTIAL.
RX Clin. Immunol. Immunopathol. 87:184-192(1998).			VH4 HEAVY CHAIN VARIABLE REGION.
RX -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			VH4 HEAVY CHAIN VARIABLE REGION.
CC DOMAIN			VH4 HEAVY CHAIN VARIABLE REGION.
DR EMBL; AF035041; AAD56277.1; -.			Query Match 58.7%; Score 435.5; DB 4; Length 150;
DR InterPro; IPR03006; Ig_MHC.			Best Local Similarity 64.6%; Pred. No. 4.8e-36; Indels 9; Gaps 3;
DR InterPro; IPR03596; Ig_v.			Matches 93; Conservative 15; Mismatches 27;
DR Pfam; PF00047; ig; Ig_v.			Indels 9; Gaps 3;
DR SMART; SM00406; IgV; Ig_v.			Query Match 58.7%; Score 435.5; DB 4; Length 150;
FT NON_TER 1 1			Best Local Similarity 64.6%; Pred. No. 4.8e-36; Indels 9; Gaps 3;
FT NON_TER 119 119			Matches 93; Conservative 15; Mismatches 27;
FT NON_TER 119 119 MW; 1BDB86B6420FA0BE CRC64;			Indels 9; Gaps 3;
SEQUENCE 119 AA; 13219 MW;			Query Match 58.7%; Score 435.5; DB 4; Length 150;
Q9BU10	PRELIMINARY;	PRT;	Best Local Similarity 64.6%; Pred. No. 4.8e-36; Indels 9; Gaps 3;
ID Q9BU10	PRELIMINARY;	PRT;	Matches 93; Conservative 15; Mismatches 27;
AC 03B010;			Indels 9; Gaps 3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)			Query Match 58.9%; Score 437; DB 4; Length 119;
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)			Matches 88; Conservative 11; Mismatches 16; Indels 12; Gaps 2;
DE UNKNOWN (PROTEIN FOR MGIC:1652).			Query Match 58.9%; Score 437; DB 4; Length 119;
OS Homo sapiens (Human);			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Matches 88; Conservative 11; Mismatches 16; Indels 12; Gaps 2;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Query Match 58.9%; Score 437; DB 4; Length 119;
NCBI_TAXID=9606;			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;
OX			Matches 88; Conservative 11; Mismatches 16; Indels 12; Gaps 2;
RP SEQUENCE FROM N.A.			Query Match 58.9%; Score 437; DB 4; Length 119;
RC TISSUE=LYMPHOMA;			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;
RA Submits (FEB 2001) to the EMBL/GenBank/DBJ databases.			Matches 88; Conservative 11; Mismatches 16; Indels 12; Gaps 2;
DR EMBL; BC002963; AAH02963.1; -.			Query Match 58.9%; Score 437; DB 4; Length 119;
SEQUENCE 597 AA; 65274 MW;			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;
Q9BQ8	PRELIMINARY;	PRT;	Matches 93; Conservative 15; Mismatches 27;
ID Q9BQ8	PRELIMINARY;	PRT;	Indels 12; Gaps 2;
AC Q9BQ8;			Query Match 58.9%; Score 437; DB 4; Length 119;
DT 01-JUN-2001 (TREMBLrel. 17, Created)			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;
DE VH4 HEAVY CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).			Matches 88; Conservative 11; Mismatches 16; Indels 12; Gaps 2;
GN IGM.			Query Match 58.9%; Score 437; DB 4; Length 119;
OS Homo sapiens (Human).			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Matches 88; Conservative 11; Mismatches 16; Indels 12; Gaps 2;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Query Match 58.9%; Score 437; DB 4; Length 119;
NCBI_TAXID=9606;			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;
RN [1]	SEQUENCE FROM N.A.		Matches 88; Conservative 11; Mismatches 16; Indels 12; Gaps 2;
RP Suh, C.-H., Song, C.-H., Lee, C.-H., Lee, S.-K.;			Query Match 58.9%; Score 437; DB 4; Length 119;
RP "Clonal proliferation of IgM secreting B cell in the synovium of			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;
RP Behcet's patient with arthritis";			Matches 88; Conservative 11; Mismatches 16; Indels 12; Gaps 2;
RP Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases			Query Match 58.9%; Score 437; DB 4; Length 119;
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.			Best Local Similarity 69.3%; Pred. No. 2.6e-36; Indels 12; Gaps 2;

DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
OS	UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;		
OX	NCBI_TaxID=9606;		
RN	RP	SEQUENCE FROM N.A.	
RC	RC	TISSUE=RHABDOMYOSARCOMA;	
RA	RA	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	
RN	RN	SEQUENCE FROM N.A.	
RC	RC	TISSUE=LYMPHOA;	
RA	RA	Strausberg R.; Strausberg R.;	
RL	RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	
DR	DR	EMBL; BC006180; AAH06180 1; -.	
DR	DR	EMBL; BC001872; AAH01872 1; -.	
DR	DR	SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;	
Query Match	57 5%; Score 427; DB 4; Length 597; Best Local Similarity 62.4%; Pred. No. 1.6e 34; Matches 93; Conservative 11; Mi smatches 33; Indels 12; Gaps 2;		
QY	1 MAVLYFLCLVAAFPSCVLSQLQESGPQLVKPSQTLSTCTVSGFSLTSYGYWVROPP 60		
Db	1 MKHLMFELLVLVAAPRWLSQLVQQWAGLLKPSQTSLSLTCGYGGSPSYWVROPP 60		
QY	61 GKGLEWLGTYWAGGTNNYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYCARGPFP 120		
Db	61 GKGLEWLGINHSCITNNYNSPLSKRSRVTLSVDTSKQSLKSSVNAADTAVYCAR -- 116		
QY	121 AMMKRGK --- YAMDYWGQGTLYVSS 142		
Db	117 -VTRASPGTDGRYGMDWGQGTTVTVSS 144		
RESULT	6		
Q93M22	PRELIMINARY;		
ID	Q93M22		
AC	Q93M22;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	UNKNOWN (PROTEIN FOR MGC:6342).		
CA	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	RP	SEQUENCE FROM N.A.	
RC	RC	TISSUE=MAMMARY TUMOR;	
RA	RA	Strausberg R.;	
RL	RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	
DR	DR	EMBL; BC002091; AAH02091 1; -.	
SEQUENCE	479 AA; 51992 MW; 768E39A136918892 CRC64;		
Query Match	52.9%; Score 392.5; DB 11; Length 479; Best Local Similarity 5.6%; Pred. No. 3.5e-31; Matches 85; Conservative 18; Mi smatches 29; Indels 13; Gaps 5;		
QY	1 MAVLYFLCLVAAFPSCVLSQLQESGPQLVKPSQTSLSLTCVGFSLTSYGYV -WVRQ 58		
Db	1 MKVLSLLYLTAIPG -LTSVQLOQESGPQLVKPSQTSLSLTCVGFSLTSYGYV -WVRQ 58		
QY	59 PPGKLGEWLGTYWAGGTNNYNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYCARGP 118		
Db	59 FPGNKLWGMGINYDGSNNVNPNSLKRISTRDTSKNQVSLKSSVTAADTAVYCARGP 115		
QY	119 PHAMMKRGYAMDYWGQGTLYVSS 142		
Db	116 ----SRGYSWFPNQGQGTLYVSSA 135		
RESULT	7		
Q9UL96	PRELIMINARY;		
ID	Q9UL96;		
AC	Q9UL96;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
RN	RP	SEQUENCE FROM N.A.	
RX	RX	Medline=98277139; PubMed=9614934;	
RA	RA	Wu X.; Liu B.; Van der Merwe P.L.; Kalis N.N.; Berney S.M.; Young D.C.;	
RA	RA	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus." Clin. Immunol. Immunopathol. 87:184-192(1998).	
CC	CC	- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
CC	CC	EMBL; AF035018; AAD56254 1; -.	
DR	DR	InterPro; IPR030006; Ig_MHC.	
DR	DR	InterPro; IPR03596; Ig_v.	
DR	DR	PF00047; ig; 1.	
DR	DR	SMART; SMO0406; Ig_v; 1.	
FT	FT	NON_TER 1 1.	
FT	FT	NON_TER 121 121.	
SQ	SQ	SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;	
Query Match	50.4%; Score 374; DB 4; Length 121; Best Local Similarity 60.8%; Pred. No. 5.2e-30; Matches 76; Conservative 14; Mi smatches 29; Indels 6; Gaps 7;		
QY	20 QVOLQESGPGLVVKPQTSQTSLSLCTVSGFSLTSYGYVWAGGGTN 77		
Db	20 QVTLKESGPPLVVKPQTSQTSLSLCTVSGFSLTSYGYVWAGGGTN 77		
QY	78 YNSALMSRATISKDTSKNQVSLKSSVTAADTAVYCARGPMMKRGYAMDYWGQSTL 137		
Db	61 YSPSLKSLRSLTISKDTSKNQVSLTMTFMPDPWDTATYCA ---HRKSGDGYFDYWGQSTL 116		
QY	138 VTVSS 142		
Db	117 VTVSS 121		
RESULT	8		
Q9UL75	PRELIMINARY;		
ID	Q9UL75;		
AC	Q9UL75;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
RN	RN	SEQUENCE FROM N.A.	
RP	RP	SEQUENCE FROM N.A.	
RX	RX	Medline=98277139; PubMed=9614934;	
RA	RA	Wu X.; Liu B.; Van der Merwe P.L.; Kalis N.N.; Berney S.M.; Young D.C.;	
RA	RA	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus." Clin. Immunol. Immunopathol. 87:184-192(1998).	



CC	DOMAIN								
DR	EMBL; AF035024; AAD56260.1;								
DR	Intertiro; IPR003006; Ig_MHC.								
DR	IPR033596; Ig_V.								
Pfam	PF00047; ig_1.								
SMART	SM00406; IgV_1.								
FT	NON_TER	1							
FT	NON_TER	113	113						
SQ	SEQUENCE	113 AA;	12437 MW;	ED57FDD19086D07F	CRC64;				
						Db	121 WGQGTLYTVSS	131	
						RESULT	13		
						ID	Q9UL71		
						AC	Q9UL71;	PRELIMINARY;	
								PRT;	
								121 AA.	
Query Match	43.5%	Score 323;	DB 4;	Length 113;		DT	01-MAY-2000	(TREMBLrel. 13, Created)	
Best Local Similarity	50.8%	Pred. No. 6.1e-25;				DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
Matches	63;	Conservative	22;	Mismatches	27;	DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)	
Qy	20	QVQLESGGLVKPQSPQSLTCTVGSFLTSYGVYWWQPGKGLEWLGIVI-WAGTTNY	78			DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).		
Db	1	EVOLVESGGVYVQPGGSLRLSCAASGFTTSSYGMHWRQAGKGLEWATVTRYDSKNYK	60			OS	Homo sapiens (Human).		
						OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
						OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
						RA	Wu X., Liu B., Van der Merve P.L., Kalis N.N., Berney S.M.,		
						RA	Young D.C.,		
						RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal		
						RT	fetus."		
						RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
						CC	-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
						CC	DOMAIN		
						DR	EMBL; AF035043; AAD56279.1;	-.	
						DR	HSSP; P01772; 2FBA.		
						DR	InterPro; IPR003006; Ig_MHC.		
						DR	InterPro; IPR003516; Ig_v.		
						DR	SMART; SM00406; IgV; 1.		
						FT	NON_TER	1	
						FT	NON_TER	121	
						SQ	SEQUENCE	121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;	
Query Match	43.3%	Score 321;	DB 4;	Length 121;					
Best Local Similarity	50.8%	Pred. No. 1e-24;				Matches	63;	Conservative	
Matches	63;	Mismatches	22;	Mismatches	35;	Indels	4;	Gaps	
Qy	20	QVQLESGGLVKPQSPQSLTCTVGSFLTSYGVYWWQPGKGLEWLGIVI-GGTTNY	78			Qy	20	QVQLESGGLVKPQSPQSLTCTVGSFLTSYGVYWWQPGKGLEWLGIVI-GGTTNY	78
Db	1	EVQLVESGGVQVQPGSRLRFCAASGFTEDGYAMHWVQAPGKGLEWNSLSSDGGSTYY	60			Db	1	EVQLVESGGVQVQPGSRLRFCAASGFTEDGYAMHWVQAPGKGLEWNSLSSDGGSTYY	60
						Qy	79	NSALMSRATISKDTSKNQVSLKLESSVTADTAVYYCARGPPHAMMKGARYMDWGOGLT	138
						Db	61	ADSVKGRFTISDRNSKNSLYLQNSNLRADTALYCAKGKVTTIYDR--FDIWGQSTMV	117
						Qy	139	TVSS 142	
						Db	118	TVSS 121	
Query Match	43.3%	Score 321;	DB 4;	Length 121;					
Best Local Similarity	50.8%	Pred. No. 1e-24;				Matches	63;	Conservative	
Matches	63;	Mismatches	22;	Mismatches	35;	Indels	4;	Gaps	
Qy	20	QVQLESGGLVKPQSPQSLTCTVGSFLTSYGVYWWQPGKGLEWLGIVI-GGTTNY	78			Qy	20	QVQLESGGLVKPQSPQSLTCTVGSFLTSYGVYWWQPGKGLEWLGIVI-GGTTNY	78
Db	1	EVQLVESGGVQVQPGSRLRFCAASGFTEDGYAMHWVQAPGKGLEWNSLSSDGGSTYY	60			Db	1	EVQLVESGGVQVQPGSRLRFCAASGFTEDGYAMHWVQAPGKGLEWNSLSSDGGSTYY	60
						Qy	79	NSALMSRATISKDTSKNQVSLKLESSVTADTAVYYCARGPPHAMMKGARYMDWGOGLT	138
						Db	61	ADSVKGRFTISDRNSKNSLYLQNSNLRADTALYCAKGKVTTIYDR--FDIWGQSTMV	117
						Qy	139	TVSS 142	
Query Match	43.5%	Score 323;	DB 4;	Length 131;					
Best Local Similarity	50.4%	Pred. No. 7.2e-25;				Matches	66;	Conservative	
Matches	66;	Mismatches	23;	Mismatches	34;	Indels	8;	Gaps	
Qy	20	QVQLESGGLVKPQSPQSLTCTVGSFLTSYGVYWWQPGKGLEWLGIVI--GGTT	76			Qy	77	NYNSALMSRATISKDTSKNQVSLKLESSVTADTAVYYCARGPPHAM---	131
Db	1	EVQLVESGGVQVQPGSRLRFCAASGFTEDGYAMHWVQAPGKGLEWNSLSSDGGSTYY	60			Db	61	DAAPVKGRFTISDRNSKNTLRLRMSNLKTEAVYYCARGPPHAM---	131
						Qy	132	WGQGTLYTVSS	142

